

G. KAUSHAL

#6/30

1633

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JAN 26 2001

TECH CENTER 1600/2300

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/578,900

DATE: 01/11/2001
TIME: 11:39:39

Input Set : A:\019 Sequence Listing.txt
Output Set: N:\CRF3\01112001\I578900.raw

5 <110> APPLICANT: John P. Carulli et al.
7 <120> TITLE OF INVENTION: REGULATING LIPID LEVELS VIA THE ZMAX1 & HBM GENE
9 <130> FILE REFERENCE: 032796-019
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/578,900
C--> 11 <141> CURRENT FILING DATE: 2000-05-26
11 <150> PRIOR APPLICATION NUMBER: Unassigned
13 <151> PRIOR FILING DATE: 2000-05-26
15 <150> PRIOR APPLICATION NUMBER: US 09/543,771
17 <151> PRIOR FILING DATE: 2000-04-05
19 <150> PRIOR APPLICATION NUMBER: US 09/544,398
21 <151> PRIOR FILING DATE: 2000-04-05
23 <160> NUMBER OF SEQ ID NOS: 62
26 <210> SEQ ID NO: 1
28 <211> LENGTH: 5120
30 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
36 <400> SEQUENCE: 1
40 actaaagcgc gcgcgcgcgc ccattggagcc cgagtgagcg cggcgccggc ccgtccggcc 60
42 gccggacaac atg gag gca gcg ccg ccc ggg ccg ccg tgg ccg ctg ctg 109
44 Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu
46 1 5 10
48 ctg ctg ctg ctg ctg ctg ctg ggc tgc gcc tgc ccg gcc ccc gcc 157
50 Leu Leu Leu Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala
52 15 20 25
54 gcg gcc tgc ccg ctg ctg ctg ttt gcc aac cgc cgg gac gta cgg ctg 205
56 Ala Ala Ser Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu
58 30 35 40 45
60 gtg gac gcc gcc gga gtc aag ctg gag tcc acc atc gtg gtc agc gcc 253
62 Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly
64 50 55 60
66 ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg 301
68 Leu Glu Asp Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val
70 65 70 75
72 tgc tgg aca gac gtg agc gag gag gcc atc aag cag acc tgc ctg aac 349
74 Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn
76 80 85 90
78 cag acg ggg gcc gcc gtc cag aac gtg gtc atc tcc gcc ctg gtc tct 397
80 Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser
82 95 100 105
84 ccc gac gcc ctg gcc Lgc gac Lgg gtc gcc aag aag ctg tgc tgg acg 445
86 Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr
88 110 115 120 125
90 gac tca gag acc aac cgc atc gag gtc gcc aac ctg aat gcc aca tcc 493
92 Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser
94 130 135 140
96 cgg aag gtc ctg ttc tgg cag gac ctt gac cag ccg agg gcc atc gcc 541
98 Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala

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100	145	150	155	
102	ttg gac ccc gct cac ggg tac atg tac tgg aca gac tgg ggt gag acg			589
104	Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr			
106	160	165	170	
108	ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att			637
110	Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile			
112	175	180	185	
114	gtg gac tgg gac att tac tgg ccc aat gga ctg acc atc gac ctg gag			685
116	Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu			
118	190	195	200	205
120	gag cag aag ctg tac tgg gct gac gcc aag ctg agc ttc atc cac cgt			733
122	Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg			
124	210	215	220	
126	gcc aac ctg gac ggc tgg ttc cgg cag aag gtg gtg gag ggc agc ctg			781
128	Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu			
130	225	230	235	
132	acg cac ccc ttc gcc ctg acg ctg tcc ggg gac act ctg tac tgg aca			829
134	Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr			
136	240	245	250	
138	gac tgg cag acc cgc tcc atc cat gcc tgc aac aag cgc act ggg ggg			877
140	Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly			
142	255	260	265	
144	aag aag aag gag atc ctg agt gcc ctg tac tca ccc atg gac atc cag			925
146	Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Glu			
148	270	275	280	285
150	gtg ctg agc cag gag cga cag cct ttc ttc cac act cgc tgt gag gag			973
152	Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu			
154	290	295	300	
156	gac aat ggc agc tgc tcc cac ctg tgc ctg ctg tcc cca agc gag cct			1021
158	Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro			
160	305	310	315	
162	ttc tac aca tgc gcc tgc ccc acg ggt gtg cag ctg cag gac aac ggc			1069
164	Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly			
166	320	325	330	
168	agg acg tgt aag gca gga gcc gag gag gtg ctg ctg ctg gcc cgg cgg			1117
170	Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Ala Arg Arg			
172	335	340	345	
174	acg gac cta cgg agg atc tgg ctg gac acg cgg gac ttc acc gac atc			1165
176	Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile			
178	350	355	360	365
180	gtg ctg cag gtg gac gac atc cgg cac gcc att gcc atc gac tac gac			1213
182	Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp			
184	370	375	380	
186	cgg cta gag ggc tat atc tac tgg aca gat gac gag gtg cgg gcc atc			1261
188	Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile			
190	385	390	395	
192	cgc agg ggg tac ctg gac ggg tct ggg ggg cag acg ctg gtc aac acc			1309
194	Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Glu Thr Leu Val Asn Thr			
196	400	405	410	

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198	gag atc aac gac ccc gat ggc atc ggc gtc gac tgg gtg gcc cga aac	1357
200	Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn	
202	415 420 425	
204	etc tac tgg acc gac acg ggc acg gac cgc atc gag gtg acg cgc etc	1405
206	Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu	
208	430 435 440 445	
210	aac gac acc tcc cgc aag atc ctg gtg tcc gag gac ctg gac gag ccc	1453
212	Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro	
214	450 455 460	
216	cga gcc atc gca ctg cac ccc gtg atg ggc etc atg tac tgg aca gac	1501
218	Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp	
220	465 470 475	
222	tgg gga gag aac cct aaa atc gag tgt gcc aac ttg gat ggg cag gag	1549
224	Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu	
226	480 485 490	
228	cgg cgt gtg ctg gtc aat gcc tcc etc ggg tgg ccc aac ggc ctg gcc	1597
230	Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala	
232	495 500 505	
234	ctg gac ctg cag gag ggg aag etc tac tgg gga gac gcc aag aca gac	1615
236	Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp	
238	510 515 520 525	
240	aag atc gag gtg atc aat gtl gat ggg acg aag aag cgg acc etc ctg	1693
242	Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu	
244	530 535 540	
246	gag gac aag etc ccc cac att ttc ggg ttc acg ctg ctg ggg gac ttc	1741
248	Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe	
250	545 550 555	
252	atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag	1789
254	Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys	
256	560 565 570	
258	gtc aag gcc agc cgg gac gtc atc att gac cag ctg ccc gac ctg atg	1837
260	Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met	
262	575 580 585	
264	ggg etc aaa gct gtg aat gtg gcc aag gtc gtc gga acc aac cgg tgt	1885
266	Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys	
268	590 595 600 605	
270	ggg gac aag aac ggg ggg tgc agc cac ctg tgc ttc ttc aca ccc cac	1933
272	Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His	
274	610 615 620	
276	gga acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg aqt gac atg	1981
278	Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met	
280	625 630 635	
282	aag acc tgc atc gta cct gag gcc ttc ttg gtc etc acc agc aga gcc	2029
284	Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala	
286	640 645 650	
288	gcc atc cac aag atc tcc etc gag acc aat aac aac gac gtg gcc atc	2077
290	Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile	
292	655 660 665	
294	ccg etc acg ggc gtc aag gag gcc tca gcc ctg gac tll gat gtg tcc	2125

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296	Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser	685	
298	670	675	680
300	aac aac cac atc tac tgg aca gac gtc agc ctg aag acc atc agc cgc		2173
302	Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg		
304	690	695	700
306	gcc ttc atg aac ggg agc tgc gtg gag cac gtg gtg gag ttt ggc ctt		2221
308	Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu		
310	705	710	715
312	gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac		2269
314	Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr		
316	720	725	730
318	tgg gcc gac act ggg acc aac aca atc gaa gtg gcg cgg ctg gac ggg		2317
320	Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly		
322	735	740	745
324	cag ttc cgg caa gtc ctc gtg tgg agg gac ttg gac aac ccg agg tgc		2365
326	Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser		
328	750	755	760
330	ctg gcc ctg gat ccc acc aag ggc tac atc tac tgg acc gag tgg ggc		2413
332	Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly		
334	770	775	780
336	ggc aag ccg agg atc gtg cgg gcc ttc atg gac ggg acc aac tgc atg		2461
338	Gly Lys Pro Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met		
340	785	790	795
342	acg ctg gtg gac aag gtg ggc cgg gcc aac gac ctc acc att gac tac		2509
344	Thr Leu Val Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr		
346	800	805	810
348	gct gac cag cgc ctc tac tgg acc gac ctg gac acc aac atg atc gag		2557
350	Ala Asp Gln Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu		
352	815	820	825
354	tgc tcc aac atg ctg ggt cag gag cgg gtc gtg att gcc gac gat ctc		2605
356	Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu		
358	830	835	840
360	ccg cac ccg ttc ggt ctg acg cag tac agc gat tat atc tac tgg aca		2653
362	Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr		
364	850	855	860
366	gac tgg aat ctg cac agc att gag cgg gcc gac aag act agc ggc cgg		2701
368	Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg		
370	865	870	875
372	aac cgc acc ctc atc cag ggc cac ctg gac ttc gtg atg gac atc ctg		2749
374	Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu		
376	880	885	890
378	gtg ttc cac tcc tcc cgc cag gat ggc ctc aat gac tat atg cac aac		2797
380	Val Phe His Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn		
382	895	900	905
384	aac ggg cag tat ggg cag ctg tgc ctt gcc atc ccc ggc ggc cac cgc		2845
386	Asn Gly Gln Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg		
388	910	915	920
390	tgc ggc tgc gcc tca cac tac acc ctg gac ccc agc agc cgc aac tgc		2893
392	Cys Gly Cys Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys		

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394		930		935		940		2941
396	agc	ccg	ccc	acc	ttc	ttg	ctg	ttc
398	Ser	Pro	Pro	Thr	Thr	Phe	Leu	Leu
400								
402	cgg	atg	atc	ccg	gac	gac	cag	cac
404	Arg	Met	Ile	Pro	Asp	Asp	Gln	His
406								
408	cat	gga	ctg	agg	aac	gtc	aaa	gcc
410	His	Gly	Leu	Arg	Asn	Val	Lys	Ala
412								
414	ttc	atc	tac	tgg	gtg	gat	ggg	cgc
416	Phe	Ile	Tyr	Trp	Val	Asp	Gly	Arg
418								
420	gac	ggg	acc	cag	ccc	ttt	gtt	ttg
422	Asp	Gly	Thr	Gln	Pro	Phe	Val	Leu
424								
426	cca	gac	aaq	cag	ccc	cac	gac	ctc
428	Pro	Asp	Arg	Gln	Pro	His	Asp	Leu
430								
432	ctg	ttc	tgg	acg	tgc	gag	gcc	acc
434	Leu	Phe	Trp	Thr	Cys	Glu	Ala	Thr
436								
438	agc	ggg	gaa	gcc	atg	ggg	gtg	ctg
440	Ser	Gly	Glu	Ala	Met	Gly	Val	Val
442								
444	agg	gcc	atc	gtc	gtc	aac	gcg	gag
446	Arg	Ala	Ile	Val	Val	Asn	Ala	Glu
448								
450	atg	caa	gac	cgg	gca	gcc	aaq	atc
452	Met	Gln	Asp	Arg	Ala	Ala	Lys	Ile
454								
456	gag	cgc	gag	gtc	ctc	ttc	acc	acc
458	Glu	Arg	Glu	Val	Leu	Phe	Thr	Thr
460								
462	gtg	gtg	gac	aac	aca	ctg	ggc	aag
464	Val	Val	Asp	Asn	Thr	Leu	Gly	Lys
466								
468	aaq	cgc	att	gag	agc	tgt	gac	ctg
470	Lys	Arg	Ile	Glu	Ser	Cys	Asp	Leu
472								
474	gag	gac	gcc	aac	atc	gtg	caa	cct
476	Glu	Asp	Ala	Asn	Ile	Val	Gln	Pro
478								
480	cat	ctc	tac	tgg	atc	gac	cgc	caa
482	His	Leu	Tyr	Trp	Ile	Asp	Arg	Gln
484								
486	aaq	acc	acc	ggg	gac	aaq	cgc	act
488	Lys	Thr	Thr	Gly	Asp	Lys	Arg	Thr
490								

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2676 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:2692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:3156 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:3342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:3344 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:3346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:5328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:5632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:6640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9